

SEQUENCE LISTING

<110> SOLOMON, Beka
HANAN, Eilat

<120> AGENTS AND COMPOSITIONS AND METHODS UTILIZING SAME USEFUL IN
DIAGNOSING AND/OR TREATING OR PREVENTING PLAQUE FORMING DISEASES

<130> SOLOMON=2B

<140> 09/629,971

<141> 2000-07-31

<150> US 09/473,653

<151> 1999-12-29

<150> US 60/152,417

<151> 1999-09-03

<160> 29

<170> PatentIn version 3.0

<210> 1

<211> 4

<212> PRT

<213> Artificial

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<223> synthetic peptide

<400> 1

Glu Phe Arg His

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<210> 2

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1 5 10 15

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 Leu Val Phe Phe Ala Glu Asp Val Gly Ser Asn Lys Gly Ala Ile Ile
 20 25 30
 Gly Leu Met Val Gly Gly Val Val Ile Ala Thr
 35 40

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Trp Val Leu Asp
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 1 5 10 15
 tca gtg aag att tcc tgc aag ggt tct ggc tac aca ttc act gat tat 96
 Ser Val Lys Ile Ser Cys Lys Gly Ser Gly Tyr Thr Phe Thr Asp Tyr
 20 25 30
 gct atg cac tgg gtg aag cag agt cat gca aag agt cta gag tgg att 144
 Ala Met His Trp Val Lys Gln Ser His Ala Lys Ser Leu Glu Trp Ile
 35 40 45
 gga gtt att agt act tac tat ggt gat gct agc tac aac cag aag ttc 192
 Gly Val Ile Ser Thr Tyr Tyr Gly Asp Ala Ser Tyr Asn Gln Lys Phe
 50 55 60
 aag ggc aag gcc aca atg act gta gac aaa tcc tcc agc aca gcc tat 240
 Lys Gly Lys Ala Thr Met Thr Val Asp Lys Ser Ser Ser Thr Ala Tyr
 65 70 75 80
 atg gaa ctt gcc aga ctg aca tct gag gat tct gcc atc tat tac tgt 288
 Met Glu Leu Ala Arg Leu Thr Ser Glu Asp Ser Ala Ile Tyr Tyr Cys
 85 90 95
 gca aga ggg gct act atg tcc tac ttt gac tac tgg ggc caa gtg acc 336

Ala	Arg	Gly	Ala	Thr	Met	Ser	Tyr	Phe	Asp	Tyr	Trp	Gly	Gln	Val	Thr		
			100					105					110				
acg	gtc	acc	gtc	tcc	tca	ggg	gga	ggc	ggg	tca	ggc	gga	gtt	ggc	tct	384	
Thr	Val	Thr	Val	Ser	Ser	Gly	Gly	Gly	Gly	Ser	Gly	Gly	Val	Gly	Ser		
			115				120					125					
ggc	ggg	ggc	gga	tcc	gac	atc	gag	ctc	act	cag	tct	cca	gca	atc	atg	432	
Gly	Gly	Gly	Gly	Ser	Asp	Ile	Glu	Leu	Thr	Gln	Ser	Pro	Ala	Ile	Met		
			130			135					140						
tct	gca	tct	cca	ggg	gag	aag	gtc	acc	atg	acc	tgc	agt	gcc	agc	tca	480	
Ser	Ala	Ser	Pro	Gly	Glu	Lys	Val	Thr	Met	Thr	Cys	Ser	Ala	Ser	Ser		
					150					155					160		
agt	ata	agt	tac	atg	cac	tgg	tat	cag	cag	aag	cca	ggc	acc	tcc	ccc	528	
Ser	Ile	Ser	Tyr	Met	His	Trp	Tyr	Gln	Gln	Lys	Pro	Gly	Thr	Ser	Pro		
				165				170						175			
aaa	aga	tgg	att	tat	gac	aca	tcc	aaa	ctg	gct	tct	gga	gtc	cct	gct	576	
Lys	Arg	Trp	Ile	Tyr	Asp	Thr	Ser	Lys	Leu	Ala	Ser	Gly	Val	Pro	Ala		
			180					185					190				
cgc	ttc	agt	ggc	agt	ggg	tct	ggg	acc	tct	tat	tct	ctc	aca	atc	agc	624	
Arg	Phe	Ser	Gly	Ser	Gly	Ser	Gly	Thr	Ser	Tyr	Ser	Leu	Thr	Ile	Ser		
			195				200					205					
agc	atg	gag	gct	gaa	gat	gct	gcc	act	tat	tac	tgc	cat	cag	cgg	agt	672	
Ser	Met	Glu	Ala	Glu	Asp	Ala	Ala	Thr	Tyr	Tyr	Cys	His	Gln	Arg	Ser		
			210			215					220						
agt	tac	cca	ttc	acg	ttc	gga	ggg	ggg	gcc	aag	ctg	gaa	ata	aaa		717	
Ser	Tyr	Pro	Phe	Thr	Phe	Gly	Gly	Gly	Ala	Lys	Leu	Glu	Ile	Lys			
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<210> 6
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<400> 6

Gln	Val	Lys	Leu	Gln	Glu	Ser	Gly	Ala	Glu	Leu	Val	Arg	Pro	Gly	Val		
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Ser	Val	Lys	Ile	Ser	Cys	Lys	Gly	Ser	Gly	Tyr	Thr	Phe	Thr	Asp	Tyr		
			20					25					30				
Ala	Met	His	Trp	Val	Lys	Gln	Ser	His	Ala	Lys	Ser	Leu	Glu	Trp	Ile		
			35				40					45					
Gly	Val	Ile	Ser	Thr	Tyr	Tyr	Gly	Asp	Ala	Ser	Tyr	Asn	Gln	Lys	Phe		
	50					55					60						

Lys Gly Lys Ala Thr Met Thr Val Asp Lys Ser Ser Ser Thr Ala Tyr
65 70 75 80

Met Glu Leu Ala Arg Leu Thr Ser Glu Asp Ser Ala Ile Tyr Tyr Cys
85 90 95

Ala Arg Gly Ala Thr Met Ser Tyr Phe Asp Tyr Trp Gly Gln Val Thr
100 105 110

Thr Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Val Gly Ser
115 120 125

Gly Gly Gly Gly Ser Asp Ile Glu Leu Thr Gln Ser Pro Ala Ile Met
130 135 140

Ser Ala Ser Pro Gly Glu Lys Val Thr Met Thr Cys Ser Ala Ser Ser
145 150 155 160

Ser Ile Ser Tyr Met His Trp Tyr Gln Gln Lys Pro Gly Thr Ser Pro
165 170 175

Lys Arg Trp Ile Tyr Asp Thr Ser Lys Leu Ala Ser Gly Val Pro Ala
180 185 190

Arg Phe Ser Gly Ser Gly Ser Gly Thr Ser Tyr Ser Leu Thr Ile Ser
195 200 205

Ser Met Glu Ala Glu Asp Ala Ala Thr Tyr Tyr Cys His Gln Arg Ser
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Ser Tyr Pro Phe Thr Phe Gly Gly Gly Ala Lys Leu Glu Ile Lys
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<220>
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<400> 7

Tyr Tyr Glu Phe Arg His
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<210> 8
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<220>
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Val His Glu Pro His Glu Phe Arg His Val Ala Leu Asn Pro Val
1 5 10 15

<210> 9
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Lys Leu His
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<212> DNA
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<211> 24
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<210> 12
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38

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<211> 58

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58

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52

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His Gln Arg Ser Ser Tyr Pro Cys Thr

1

5

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His Gln Arg Ser Ser Tyr Pro Cys Thr

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5

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His Gln Arg Ser Ser Tyr Pro Phe Thr
1 5

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His Gln Arg Ser Ser Tyr Pro Tyr Thr
1 5

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His Gln Arg Ser Ser Tyr Pro Phe Thr
1 5

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His Gln Arg Ser Ser Tyr Pro Ser Thr
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Asp	Thr	Glu	Phe	Arg	His	Ser	Ser	Asn	Asn	Phe	Ser	Ala	Val	Arg
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Ser	Ala	Ala	Asp	Phe	Arg	His	Gly	Ser	Pro	Pro	Ile	Ser	Ala	Phe
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Lys Thr Asn Met Lys His Met Ala Gly Ala Ala Ala Ala Gly Ala Val


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Val Gly Gly Leu Gly
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ctc act cag tct cca gca atc atg tct gca tct cca ggg gag aag gtc      96
Leu Thr Gln Ser Pro Ala Ile Met Ser Ala Ser Pro Gly Glu Lys Val
              20              25              30

acc atg acc tgc agt gcc agc tca agt ata agt tac atg cac tgg tat      144
Thr Met Thr Cys Ser Ala Ser Ser Ser Ile Ser Tyr Met His Trp Tyr
              35              40              45

cag cag aag cca ggc acc tcc ccc aaa aga tgg att tat gac aca tcc      192
Gln Gln Lys Pro Gly Thr Ser Pro Lys Arg Trp Ile Tyr Asp Thr Ser
              50              55              60

aaa ctg gct tct gga gtc cct gct cgc ttc agt ggc agt ggg tct ggg      240
Lys Leu Ala Ser Gly Val Pro Ala Arg Phe Ser Gly Ser Gly Ser Gly
65              70              75              80

acc tct tat tct ctc aca atc agc agc atg gag gct gaa gat gct gcc      288
Thr Ser Tyr Ser Leu Thr Ile Ser Ser Met Glu Ala Glu Asp Ala Ala
              85              90              95

act tat tac tgc cat cag cgg agt agt tac cca ttc acg ttc gga ggg      336
Thr Tyr Tyr Cys His Gln Arg Ser Ser Tyr Pro Phe Thr Phe Gly Gly
              100              105              110

ggg gcc aag ctg gaa ata aaa      357
Gly Ala Lys Leu Glu Ile Lys

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115

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Gly Gly Ser Gly Gly Val Gly Ser Gly Gly Gly Ser Asp Ile Glu
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Leu Thr Gln Ser Pro Ala Ile Met Ser Ala Ser Pro Gly Glu Lys Val
20 25 30

Thr Met Thr Cys Ser Ala Ser Ser Ile Ser Tyr Met His Trp Tyr
35 40 45

Gln Gln Lys Pro Gly Thr Ser Pro Lys Arg Trp Ile Tyr Asp Thr Ser
50 55 60

Lys Leu Ala Ser Gly Val Pro Ala Arg Phe Ser Gly Ser Gly Ser Gly
65 70 75 80

Thr Ser Tyr Ser Leu Thr Ile Ser Ser Met Glu Ala Glu Asp Ala Ala
85 90 95

Thr Tyr Tyr Cys His Gln Arg Ser Ser Tyr Pro Phe Thr Phe Gly Gly
100 105 110

Gly Ala Lys Leu Glu Ile Lys
115

<210> 29
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<212> PRT
<213> Mus sp.

<400> 29

Lys Thr Asn Leu Lys His Val Ala Gly Ala Ala Ala Ala Gly Ala Val
1 5 10 15

Val Gly Gly Leu Gly
20